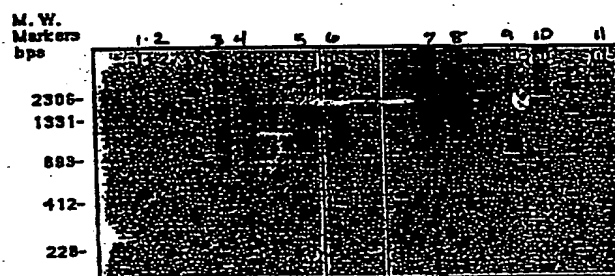
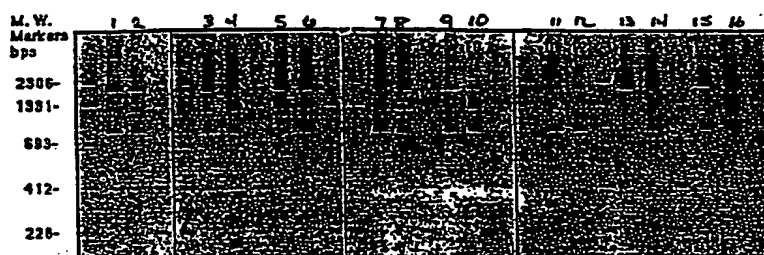




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(54) Title: USE OF A SPECIFIC MARKER FOR DETECTION OF *SALMONELLA* WITH PCR

(57) Abstract

A method is provided for the selection of diagnostic genetic markers fragments and useful in the identification of bacteria at the genus, species or serotype level. The method first involves the identification of a RAPD polymorphic DNA fragment common to a particular microbial group, the identification of the most conserved regions of that fragment, and the preparation of specific primers useful for detecting the presence of a marker within the fragment whereby that set of primers is then useful in the identification of all members of the chosen microbial group. Also provided is a specific diagnostic marker for *Salmonella* and primers directed thereto.

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TITLE

Use of a specific marker for detection of *Salmonella* with PCR.

5

FIELD OF INVENTION

The invention relates to the field of molecular biology and the use of randomly amplified nucleic acid fragments for the selection of genetic markers useful in the identification of bacteria at the genus, species or serotype level. This invention further relates to a specific DNA marker sequence useful for the detection of *Salmonella*, and use of that diagnostic marker to determine if an unknown bacterium is a member of the genus *Salmonella*.

15

BACKGROUND

An integral aspect of the field of microbiology is the ability to positively identify microorganisms at the level of genus, species or serotype. Correct identification is not only an essential tool in the laboratory but plays a significant role in the control of microbial contamination in the processing of food stuffs, production of agricultural products and monitoring of environmental media such as ground water. Increasing stringency in regulations which apply to microbial contamination have resulted in a corresponding increase in industry resources which must be dedicated to contamination monitoring.

Of greatest concern is the detection and control of pathogenic microorganisms. Although a broad range of microorganisms have been classified as pathogenic, attention has primarily focused on a few bacterial groupings such as *Escherichia*, *Salmonella*, *Listeria* and *Clostridia*. Typically, pathogen identification has relied on methods for distinguishing phenotypic aspects such as growth or motility characteristics, and

immunological and serological characteristics.

Selective growth procedures and immunological methods are the traditional methods of choice for bacterial identification, and can be effective for the presumptive
5 detection of a large number of species within a particular genus. However, these methods are time consuming, and are subject to error. Selective growth methods require culturing and subculturing in selective media, followed by subjective analysis by an experienced
10 investigator. Immunological detection (e.g., ELISA) is more rapid and specific, however it still requires growth of a significant population of organisms and isolation of the relevant antigens. For these reasons interest has turned to detection of bacterial pathogens
15 on the basis of nucleic acid sequence.

It is well known, for example, that nucleic acid sequences associated with the ribosomes of bacteria are often highly conserved across genera and are therefore useful for identification (Webster, U.S. 4,717,653 and
20 U.S. 5,087,558; Enns, Russel K. *Lab. Med.*, 19, 295, (1998); Mordarski, M. *Soc. Appl. Bacteriol. Tech. Ser.*, 20 (Chem. Methods Bact. Syst.), 41, (1985)). Weisburg et al., (EP 51736) disclose a method for the detection and identification of pathogenic microorganisms
25 involving the PCR amplification and labeling of a target nucleotide for hybridization to 16S rDNA of *E. coli*. and Lane et al., (WO 9015157) teach universal nucleic acid probes that hybridize to conserved regions of 23S or 16S rRNA of eubacteria.

30 Although bacterial ribosomal nucleic acids contain highly conserved sequences, they are not the only sources of base sequence conservation that is useful for microorganism identification. Wheatcroft et al., (CA 2055302) describe the selection of transposable
35 elements, flanked by unique DNA sequences for the

detection of various *Rhizobium* strains. Similarly Tommassen et al., (WO 9011370) disclose polynucleotide probes and methods for the identification and detection of gram-positive bacteria. The method of Tommassen et al., relies on probes corresponding to relatively short fragments of the outer membrane protein OmpA, known to be highly conserved throughout gram-positive genera. Atlas et al., (EP 517154) teach a nucleic acid hybridization method for the detection of *Giardia* sp. based on designing probes with sequences complementary to regions of the gene encoding the giardin protein. Webster, J. A., (U.S. 4717653) has expanded upon the use of rRNA in disclosing a method for the characterization of bacteria based on the comparison of the chromatographic pattern of restriction endonuclease-digested DNA from the unknown organism with equivalent chromatographic patterns of at least 2 known different organism species. The digested DNA has been hybridized or reassociated with ribosomal RNA information-containing nucleic acid from, or derived from a known probe organism. The method of Webster et al., effectively establishes a unique bacterial nucleic acid "fingerprint" corresponding to a particular bacterial genus against which unknown "fingerprints" are compared.

25 The methods described above are useful for the detection of bacteria but each relies upon knowledge of a gene, protein, or other specific sequence known a priori to be highly conserved throughout a specific bacterial group. An alternative method would involve a nontargeted analysis of bacterial genomic DNA for specific non-phenotypic genetic markers common to all species of that bacteria. For example, genetic markers based on single point mutations may be detected by differentiating DNA banding patterns from restriction enzyme analysis. As restriction enzymes cut DNA at

specific sequences, a point mutation within this site results in the loss or gain of a recognition site, giving rise in that region to restriction fragments of different length. Mutations caused by the insertion, deletion or inversion of DNA stretches will also lead to a length variation of DNA restriction fragments. Genomic restriction fragments of different lengths between genotypes can be detected on Southern blots (Southern, E. M., *J. Mol. Biol.* 98, 503, (1975). The genomic DNA is typically digested with any restriction enzyme of choice, the fragments are electrophoretically separated, and then hybridized against a suitably labelled probe for detection. The sequence variation detected by this method is known as restriction length polymorphism or RFLP (Botstein et al. *Am. J. Hum. Genet.* 342, 314, (1980)). RFLP genetic markers are particularly useful in detecting genetic variation in phenotypically silent mutations and serve as highly accurate diagnostic tools.

Another method of identifying genetic polymorphic markers employs DNA amplification using short primers of arbitrary sequence. These primers have been termed 'random amplified polymorphic DNA', or "RAPD" primers, Williams et al., *Nucl. Acids. Res.*, 18, 6531 (1990) and U.S. 5,126,239; (also EP 0 543 484 A2, WO 92/07095, WO 92/07948, WO 92/14844, and WO 92/03567). The RAPD method amplifies either double or single stranded nontargeted, arbitrary DNA sequences using standard amplification buffers, dATP, dCTP, dGTP and TTP and a thermostable DNA polymerase such as *Taq*. The nucleotide sequence of the primers is typically about 9 to 13 bases in length, between 50 and 80% G+C in composition and contains no palindromic sequences. RAPD detection of genetic polymorphisms represents an advance over RFLP in that it is less time consuming, more informative, and

readily susceptible to automation. Because of its sensitivity for the detection of polymorphisms RAPD analysis and variations based on RAPD/PCR methods have become the methods of choice for analyzing genetic variation within species or closely related genera, both in the animal and plant kingdoms. For example, Landry et al., (*Genome*, 36, 580, (1993)) discuss the use of RAPD analysis to distinguish various species of minute parasitic wasps which are not morphologically distinct. Van Belkum et al., (*Mol. Biochem Parasitol* 61, 69, (1993)) teach the use of PCR-RAPD for the distinction of various species of *Giardi*.

In commonly assigned application USSN 07/990,297, Applicants disclose a method of double-nested PCR which is used to detect the presence of a specific microbe. This disclosure first describes identifying a random unique segment of DNA for each individual microorganism which will be diagnostic for that microorganism. To identify and obtain this diagnostic nucleic acid segment a series of polymorphic markers is generated from each organism of interest using single primer RAPD analysis. The RAPD series from each organism is compared to similarly generated RAPD series for other organisms, and a RAPD marker unique to all members of the group is then selected. The unique marker is then isolated, amplified and sequenced. Outer primers and inner primers suitable for double-nested PCR of each marker may then be developed. These primers comprise sequence segments within the RAPD markers, wherein the inner set of primers will be complementary to the 3' ends of the target piece of nucleic acid. These nested primers may then be used for nested PCR amplification to definitely detect the presence of a specific microorganism.

In the present method Applicants have more particularly adapted and more fully described this RAPD

methodology to identify a sequence, or marker; the presence of which will be diagnostic for all individuals of a genetically related population. The present method first involves a RAPD amplification of genomic DNA of a representative number of individuals within a specific genus, species or subspecies to produce a RAPD amplification product, termed the diagnostic fragment. This diagnostic fragment must be present in the RAPD profiles in over 90% of the individuals tested.

Sequence information from the diagnostic fragment will then enable identification of the most suitable PCR primer binding sites within the diagnostic fragment to define a unique diagnostic marker. Primers flanking this marker will be useful to produce an amplification product in the genetically selected group, but will not produce any amplification product in individuals outside of that group.

An important aspect of the present invention is the identification of the most conserved primer binding sites within this diagnostic sequence, which is accomplished by first determining which individuals, in the genus or grouping to be detected, exhibit the most genetic variation within the diagnostic sequence. Screening this subpopulation of "most polymorphic" individuals using various primers generated from the diagnostic sequence will define the most highly conserved primer bindings sites within the diagnostic fragment. Primers directed toward these highly conserved primer binding sites are then useful for the detection of all members of the genus, based upon the ability of the selected primers to amplify the diagnostic marker present in that particular population. A "yes" or "no" answer can then be readily provided to the question of whether a microorganism is a member of the genetically related population. If DNA

amplification occurs using these primers, the target is present and the identity is confirmed as "yes". If amplification does not occur, the answer is no; the microorganism is not a member of that genetically related population. The necessity of electrophoresis to determine the presence of a marker of any particular size is eliminated.

Applicants' method is distinctive in that to accomplish detection of a member of a group of organisms, the method first relies on determining the most conserved regions of a diagnostic fragment from a phenotypically uncharacterized segment of DNA common to all members of that group. One of skill in the art will recognize that conservation of sequence may represent both an ally and an enemy in the process of identification of the members of a particular genus. For example, many bacterial sequences are conserved across genera and hence would not be useful in the determination of species within a particular genus. It is precisely for that reason that methods heretofore elucidated in that art rely primarily on the analysis of sequences derived from proteins or genes known to be specific to a particular genus, i.e., ribosomal RNA or outer membrane proteins. Applicants' method departs from the art in that the conserved sequences of the instant method are not derived from a known gene, nor is the sequence associated with any known phenotypic characteristic. Further, Applicants' method is refined by the selection of the most conserved region of the diagnostic fragment by comparison with the genomic DNA of a subpopulation of individuals exhibiting the most genetic variation within the diagnostic fragment. Applicants' method presupposes that the regions of the diagnostic fragment most conserved within the polymorphic subpopulation will also be conserved within

the larger population comprising all members of the genus. Applicants are unaware of any art teaching this supposition.

- The process of the present invention has been
5. enabled in the present disclosure by the elucidation of a diagnostic marker sequence which is useful in rapidly and definitively identifying bacteria from the genus *Salmonella*.

SUMMARY OF THE INVENTION

- 10 The present invention provides a method for the determination of diagnostic genetic markers for the identification of individuals of a genetically related population of microorganisms. The method comprises the following steps:

- 15 (i) The first step entails performing a RAPD amplification on the genomic DNA of a representative number of individuals from a genetically related population, wherein said number of individuals will comprise the positive test panel, and whereby the RAPD
- 20 amplification performed on individuals of the positive test panel will generate a RAPD marker profile from each individual of the positive test panel. Similarly the same RAPD amplification is performed on the genomic DNA of a significant number of individuals genetically
- 25 unrelated to the positive test panel, wherein said number of genetically unrelated individuals will comprise the negative test panel, and whereby the RAPD amplification on individuals of the negative test panel will generate a RAPD marker profile from each individual
- 30 of the negative test panel.

- (ii) The second step comprises comparing the RAPD marker profiles from individuals of the positive test panel with the RAPD marker profiles from individuals of the negative test panel and thereby
- 35 selecting a diagnostic nucleic acid fragment wherein

said fragment is present in over 90% of the RAPD marker profiles from the positive test panel and absent in the RAPD marker profiles from the negative test panel.

(iii) The nucleotide sequence of said
5 diagnostic fragment is determined to identify available primer binding sites.

(iv) One or more pairs of primers
corresponding to the available primer binding sites of
step (iii) are prepared.

10 (v) Primer-directed amplification is
performed on the genomic DNA of a significant number of
individuals from the positive test panel using the
primer pairs of step (iv), whereby a subpopulation of
individuals which are the most polymorphic with respect
15 to said diagnostic fragment is identified.

(vi) Primer-directed amplification is next
performed on the genomic DNA of said polymorphic
subpopulation of (v) using several candidate primer
pairs derived from the sequence of said diagnostic
20 fragment, whereby a particular candidate primer pair
which produces primer amplification product for the
highest percentage of individuals within the polymorphic
subpopulation is thereby empirically selected. This
primer pair now defines the diagnostic marker for that
25 genetically related population of step (i).

(vii) The method further comprises the step of
confirming that the particular primer pair identified in
(vi) is useful for amplifying a diagnostic genetic
marker which is present in all of the genetically
30 related individuals while absent in all of the
genetically unrelated individuals, wherein said
confirmation is accomplished by amplifying the genomic
DNA of all individuals of the positive and negative test
panels with said particular primer pair to determine
35 that said primer pair is effective in amplifying a

diagnostic genetic marker in all individuals of the positive test panel and is ineffective in amplifying said diagnostic marker in all individuals of the negative test panel.

5 This invention further provides a method of determining whether an unknown bacterium is a member of the genus *Salmonella*, comprising analyzing the genomic DNA of said unknown bacterium to detect the presence of nucleic acid Sequence ID No. 1 or its complement,
10 No. 20. In a preferred embodiment, said analysis can be accomplished by amplification using the primer pairs of Sequence ID Nos. 15 and 19.

 This invention further provides isolated nucleic acid fragments having Sequence ID Nos. 1, 4, 14, 15, 16,
15 17, 18, 19, 10, 21 and 22.

BRIEF DESCRIPTION OF THE FIGURES

 Figure 1A is a composite photograph showing electrophoretic marker profiles of amplification products for the positive test panel of *Salmonella*
20 strains amplified with a single RAPD primer, 12CN03 (Sequence ID No. 4).

 Figure 1B is a composite photograph showing electrophoretic marker profiles of amplification products for DNA from the negative test panel comprising
25 a variety of non-*Salmonella* bacterial strains amplified with a single RAPD primer, 12CN03 (Sequence ID No. 4).

 Figure 2 is the sequence of an 811 bp *Salmonella* diagnostic nucleic acid fragment, Sequence ID No. 1, which was generated by amplification of genomic DNA
30 isolated from *Salmonella typhimurium* (ATCC 29057) with the single 12-base primer 12CN03. The complementary strand to Sequence ID No. 1 is Sequence ID No. 20. Within this 811 bp nucleic acid of Figure 2, at position No. 35 to 786, is Sequence ID No. 21 and its complement,

Sequence ID No. 22, which comprise the diagnostic marker of the invention for *Salmonella*.

Figure 3 is a composite photograph showing normal (N) and polymorphic (P) electrophoretic PCR amplification products generated from the primers 54-23/665rc-23 (Sequence ID Nos. 10/13) and primers 126-23/648rc-23 (Sequence ID Nos. 11/12) from a variety of *Salmonella* strains.

Figure 4 is a composite photograph showing PCR amplification of a variety of non-*Salmonella* strains using primer #60-26 (Sequence ID No. 15) and primer #76lrc-26 (Sequence ID No. 19).

Figure 5 is a composite photograph showing PCR amplification of a variety of *Salmonella* strains using primer #60-26 (Sequence ID No. 15) and primer #76lrc-26 (Sequence ID No. 19).

DETAILED DESCRIPTION OF THE INVENTION

As used herein the following terms may be used for interpretation of the claims and specification.

"Nucleic acid" refers to a molecule which can be single stranded or double stranded, comprising monomers (nucleotides) containing a sugar, phosphate and either a purine or pyrimidine. In bacteria, lower eukaryotes, and in higher animals and plants, "deoxyribonucleic acid" (DNA) refers to the genetic material while "ribonucleic acid" (RNA) is involved in the translation of the information from DNA into proteins.

The term "primer-directed amplification" refers to any of a number of methods known in the art that result in logarithmic amplification of nucleic acid molecules using the recognition of a specific nucleic acid sequence or sequences to initiate an amplification process. Applicants contemplate that amplification may be accomplished by any of several schemes known in this art, including but not limited to the polymerase chain

reaction (PCR) or ligase chain reaction (LCR). If PCR methodology is selected, the amplification method would include a replication composition consisting of for example, nucleotide triphosphates, two primers with
5 appropriate sequences, DNA or RNA polymerase and proteins. These reagents and details describing procedures for their use in amplifying nucleic acids are provided in U.S. Patent 4,683,202 (1987, Mullis, et al.) and U.S. Patent 4,683,195 (1986, Mullis, et al.).

10 A "diagnostic fragment" refers to a particular DNA sequence which is highly conserved amongst the individuals of a particular genetically related population, for example, a genus, species, or subspecies of bacteria. In the instant invention, the term
15 "diagnostic fragment" is used to refer to that fragment generated during RAPD amplification which is present in the RAPD profiles from a particular related group but absent in profiles from individuals outside of that group. The term "diagnostic marker" is used herein to
20 refer to that portion of the diagnostic fragment which can be targeted to produce an amplification product in only members of the related group. The diagnostic marker is not present outside the related group, and attempts to amplify the diagnostic markers in
25 individuals outside of the related group will result in no nucleic acid being amplified.

The term "primer" refers to a nucleic acid fragment or sequence that is complementary to at least one section along a strand of the sample nucleic acid,
30 wherein the purpose of the primer is to sponsor and direct nucleic acid replication of a portion of the sample nucleic acid along that string. Primers can be designed to be complementary to specific segments of a targeted sequence. In PCR, for example, each primer is
35 used in combination with another primer forming a

"primer set" or "primer pair", this pair flanks the targeted sequence to be amplified. In RAPD amplification, single arbitrary primers are used to amplify nontargeted segments of nucleic acid which are located between the primer sequence sites in opposing DNA strands. The term "primer", as such, is used generally herein by Applicants to encompass any sequence-binding oligonucleotide which functions to initiate the nucleic acid replication process.

"Diagnostic primers" will refer to primers designed with sequences complementary to primer binding sites on diagnostic marker. Diagnostic primers are useful in the convenient detection and identification of individuals of a genetically related population.

A genetically related population refers to any grouping of microorganisms possessing multiple or single phenotypic characteristics of sufficient similarity to allow said organisms to be classified as a single genus, species, or subspecies of bacteria. For purposes of the present disclosure, examples of genetically related populations include, for example, the genus *Salmonella* or the species *Listeria monocytogenus*.

A "test panel" refers to a particular group of organisms or individuals selected on the basis of their genetic similarity to each other, or their genetic dissimilarity to another group (i.e., another genus, species, subspecies). A "positive test panel" will refer to a number of individuals selected for the desired genetic similarity between those individuals, and in the instant case will be comprised of individuals included within the desired genetically related population. Examples of a positive test panel would be, for example, representative members of all the species of a particular genus (assuming that genus is the desired 'genetically related population'). Similarly, a

"negative test panel" will refer to a test panel selected on the basis of genetic diversity between its members and the members of the positive test panel. An example of a negative test panel when the positive test panel is bacteria of the genus *Salmonella*, would be bacteria and other organisms outside of the *Salmonella* genus.

The term "representative number of individuals" refers to individuals within a genetically related population which are selected such that they represent the widest possible range of biochemical, morphological and immunological attributes known to exist within the targeted genetically related population. The term "representative number of individuals", when referring to individuals genetically unrelated to the genetically related population (the negative test panel), means those microorganisms which are not included within the genetically related group but are genetically similar to that group.

The term "unknown bacterium" refers to a bacterium whose identity is unknown.

The term "derived from", with reference to an amplification primer, refers to the fact that the sequence of the primer is a fragment of the sequence from which it has been "derived". The fragment is always denoted in a 5' to 3' orientation. The useful primer sequence size range for PCR amplification is about 15 base pairs to about 30 base pairs in length.

The term "RAPD" refers to 'random amplified polymorphic DNA'. "RAPD amplification" refers to a method of single primer directed amplification of nucleic acids using short primers of arbitrary sequence to amplify nontargeted, random segments of nucleic acid. U.S. 5,126,239. "RAPD method" or "RAPD analysis" refers to a method for the detection of genetic polymorphisms

involving the nontargeted amplification of nucleic acids using short primers of arbitrary sequence, whereby the profile or pattern of 'RAPD' amplification products is compared between samples to detect polymorphisms. "RAPD primers" refers to primers of about 8 to 13 bp, of arbitrary sequence, useful in the RAPD amplification or RAPD analysis according to the instant method. The "RAPD marker profile" refers to the pattern, or fingerprint, of amplified DNA fragments which are amplified during the RAPD method and separated and visualized by gel electrophoresis.

The diagnostic marker of the invention, once identified, can be used to identify an unknown microorganism by any of several analysis methods. In the present invention, primers flanking the marker are useful to amplify the marker using PCR. Alternatively, nucleic acid probes could be developed based upon some or all of the diagnostic marker sequences and thus used to detect the presence of the marker sequence using standard hybridization and reporter methods. It is contemplated that regions of about 30 base pairs or more of the diagnostic marker, especially encompassing the primer regions could be used as sites for hybridization of diagnostic probes.

The present invention provides a method for the determination of genetic markers useful in the detection and identification of all members of a genetically related population. Examples of genetically related populations include following:

- 1) microorganisms belonging to the genus *Salmonella*
- 2) microorganisms belonging to the species *Listeria monocytogenes*
- 3) microorganisms belonging to the serotype of *Escherichia coli* designated O157:H7.

The instant method is particularly useful for the detection of specific genera, species or subspecies of bacteria which may be present either in food, human or animal body fluids or tissues, environmental media or medical products and apparatti.

To practice the instant method, a RAPD amplification, using a short arbitrary primer, is performed on the genomic DNA of at least 30 individuals from a genetically related population. These individuals are selected such that they represent the widest possible range of biochemical, morphological and immunological attributes known to exist within the targeted genetically related population. The electrophoretically resolved patterns of amplification products produced by the RAPD amplifications are then compared, in hopes of indentifying a distinctive RAPD amplification product which is present in over 90% of the individuals tested. If this product is not found when the same RAPD amplification is then performed on the genomic DNA of at least 30 strains of microorganisms which fall outside of the targeted population, then this fragment is deemed to be suitable diagnostic fragment and it is then sequenced to determine suitable primer binding sites for further analysis and primer generation. It is imperative that the most conserved regions of the diagnostic fragment be determined for the generation of useful diagnostic primers, i.e., primers which will be capable of producing an amplification product in all members of the genetically related group. Determination of the most conserved region is accomplished by first determining which individuals, in the population group to be detected, exhibit the most genetic variation within the diagnostic fragment sequence. The genomic DNA of this polymorphic subpopulation is then analyzed with several sets of PCR

primers generated from the diagnostic fragment to define the most highly conserved PCR primer bindings sites within the diagnostic fragment. Primers generated from these highly conserved primer binding sites are then
5 used in assay methods for the detection of all members of the genus. The method is more particularly described below with reference to the specific method steps as provided in the Summary of the Invention.
Selection of RAPD primers and detection of diagnostic
10 fragment in members of the positive and negative control panels, steps (i) and (ii):

Genomic DNA isolated from positive and negative test panels of microorganisms was subjected to RAPD amplification using eight 12-base primers of arbitrary
15 sequence. The positive test panel comprised 62 *Salmonella* serotypes and is described in detail in the GENERAL METHODS section below. The negative test panel consisted of a variety of 11 non-*Salmonella* species and is also described in the GENERAL METHODS section below.
20 Techniques for the isolation of genomic DNA are common and well known in the art and examples may be found in Sambrook et al., Molecular Cloning: A Laboratory Manual - volumes 1,2,3 (Cold Spring Harbor Laboratory: Cold Spring Harbor, New York.

25 RAPD primers of 12 bases in length were used because at this primer length the RAPD patterns generally contained one to five amplified DNA fragments. Use of shorter primers frequently resulted in a large number of amplification products, which made the
30 extraction of a single homogeneous fragment for sequencing much more difficult. When primers of greater than 12 bases were used a significant fraction of the bacterial strains produced no RAPD products which would have necessitated the screening of a much larger number
35 of arbitrary primers. One of the primers, designated

12CN03, was found to produce both an 800 bp and 2000 bp amplification product in over 90% of the positive test panel. 12CN03 had the sequence of TTA GTC ACG GCA (Sequence ID No. 4). Neither the 800 bp nor 2000 bp
5 fragment was seen in the amplification products of the negative test panel with primer 12CN03. Because of its shorter length it was decided to focus attention on the 800 bp fragment for further analysis and this became the *Salmonella* diagnostic fragment. Figure 2 shows this
10 fragment, wherein the top strand is shown as Sequence ID No. 1, and its complementary strand is shown as Sequence ID No. 20.

The 800 bp fragment did not appear with equal intensity in all of the *Salmonella* strains in the
15 positive test panel. Considering the extreme sensitivity of RAPD patterns to sequence polymorphisms, it is assumed that the variations in the intensity of the RAPD marker in some *Salmonella* strains was the result of a minor sequence variation in the vicinity of
20 the primer site. Considering the frequency at which the *Salmonella* fragment appeared, it could still be possible for highly conserved sequences, which are common to all members of the genus *Salmonella*, to be found between the 12CN03 priming sites flanking the 800 bp fragment.

25 Sequencing of diagnostic fragment, step (iii):

The 800 bp product for *Salmonella typhimurium* 587 (ATCC #29057) was selected for extraction and sequencing. This strain was selected because it is a well-characterized type strain and because this serotype
30 of *Salmonella* is a frequently encountered pathogenic microorganism. The amplification product was isolated by gel electrophoresis and the fragment was cut from the gel, eluted and reamplified with the 12CN03 primer to provide quantities of DNA suitable for sequencing.

35 Sequencing was accomplished using the chain-termination

method of Sanger et al. (Proc. Natl. Acad. Sci. USA 74, 5463, (1977)) using fluorescence-labeled dideoxynucleotides and the Genesis 2000™ DNA Analysis System (E. I. du Pont de Nemours and Company, 5 Wilmington, DE). The complete sequence of the 800 bp *Salmonella* diagnostic fragment is shown in Figure 2. Identification of the most highly conserved regions of the diagnostic fragment, steps (iv) and (v):

10 In order for the *Salmonella* diagnostic fragment to be useful for the detection of all members of the *Salmonella* genus, it is necessary to identify the most conserved regions (i.e., primer sites) of the diagnostic fragment. In theory, identification of the conserved regions could be accomplished by generating primers to 15 the fragment based on the known sequence and isolating and sequencing the same fragment from all members of the *Salmonella* genus. Sequencing, alignment and comparison of all the sequences would allow for the determination of the most conserved portion of the sequence. 20 Although, this approach is theoretically possible, in reality it is prohibitively time consuming and expensive. The development of a general method requires an alternate approach.

The instant method provides a more direct and rapid 25 method of identifying the most conserved regions of the diagnostic fragment, wherein the first step is the identification of a subpopulation of *Salmonella* sp. which show the greatest overall variation within the 800 bp diagnostic fragment. The strains which 30 constitute this subpopulation are referred to as "polymorphic" *Salmonella*. It must be understood that this subpopulation is defined as polymorphic only in the context of the diagnostic nucleic acid fragment shown in Figure 2 and not with respect to the classical 35 biochemical and morphological attributes, which are

commonly used to classify species. Once the members of the positive test panel that are polymorphic have been identified, these polymorphic *Salmonella* are used to screen for the most highly conserved regions of the diagnostic fragment. This approach presumed that the priming sites that are conserved among the most polymorphic *Salmonella* are also conserved in the general population of *Salmonella*.

In order to determine which *Salmonella* were "polymorphic" two sets of amplification primer pairs were arbitrarily selected from the diagnostic fragment and amplifications were carried out on DNA isolated from 740 strains of *Salmonella* representing all six subgenus groups for each of the primer sets. The initial primer sets were selected to achieve a GC content of $55 \pm 3\%$ for two pairs of primers all of which are located within 200 bases of the CN03 priming sites. Any strain of *Salmonella* which showed an amplification polymorphism was classified as a "polymorphic" *Salmonella*. The following amplification events were regarded as polymorphic when they occurred with either primer set:

- i) weak, inconsistent, or total lack of production of an amplification product
- ii) amplification products which are larger or smaller than the generally observed amplification product
- iii) the presence of more than one amplification product.

The largest single polymorphic group among the 740 strains of *Salmonella* were those which produced no amplification product with at least one of the primer pairs. However, a number of strains produced either multiple amplification products or products of a different size. Some examples of these types of polymorphic amplification events are shown in Figure 3.

From the original group of 740 *Salmonella* strains a group of 43 polymorphic *Salmonella* were selected. Selection of a diagnostic primer pair to amplify the diagnostic genetic marker, step (vi):

5 Once the subpopulation of "polymorphic" *Salmonella* was identified primers were prepared for a large number sites at both ends of the *Salmonella* fragment sequence. The initial criteria for primer selection was that the GC content of the two primers should match and that the
10 overall GC content fell in the range of $55 \pm 3\%$. The second criteria was that the pairs of primers were all located within 200 bases of the CN03 priming sites. Using these primers amplifications were carried out on genomic DNA from the polymorphic *Salmonella*. Primer
15 combinations which produced an amplification product in over 90% of the polymorphic *Salmonella* were selected for further evaluation. In such combinations, one of the primer sites was "locked" while the second priming site was moved upstream or downstream one base at a time. In
20 this way the priming site that found the highest portion of polymorphic *Salmonella* was identified and fixed. The second priming site was then "locked" and additional primers were prepared, which moved the first priming site at the other end of the *Salmonella* target sequence
25 upstream or downstream one base at a time. When the priming sites which produced an amplification product for the highest percentage of polymorphic *Salmonella* were identified, these primers were then evaluated for the entire test panel of *Salmonella* strains. Based on
30 this analysis four regions were identified as being most conserved. Within these conserved regions five primer-pair combinations were capable of producing an amplification product in $\geq 95\%$ of the polymorphic *Salmonella*. These primer combinations were selected for
35 further testing.

Confirmation of selected primer pair as a diagnostic genetic marker, step (viii):

- The selected priming sites were understood to be highly conserved among the "polymorphic" *Salmonella*.
- 5 The initial step in the final screening procedure was the determination of which, if any, priming sequences were conserved outside the genus *Salmonella*. The selectivity of the *Salmonella* primer sets was evaluated using a negative test panel consisting of over 100
- 10 strains representing 28 species which were either similar phenotypically to *Salmonella* or likely to be found in similar environments. The primer combination which showed the lowest rate of false positive responses in the negative test panel was then evaluated to
- 15 determine its inclusivity for a positive test panel consisting of over 1480 *Salmonella* strains.

EXAMPLES

GENERAL METHODS

- Suitable methods of genetic engineering employed
- 20 herein are described in Sambrook et al., Molecular Cloning: A Laboratory Manual - volumes 1,2,3 (Cold Spring Harbor Laboratory: Cold Spring Harbor, New York, 1989), and in the instructions accompanying commercially available kits for genetic engineering. GeneClean
- 25 (Bio101 LaJolla, CA) was used to isolate nucleic acid fragments from agarose gels and to remove enzymes from restriction digests and was performed as specified by the manufacturer. Unless otherwise specified all other standard reagents and solutions used in the following
- 30 examples were supplied by J. T. Baker Co. (Phillipsburg, NJ).

Construction of Positive and Negative Test Panels

- For the identification of a genus level *Salmonella* RAPD marker a positive test panel consisting of a
- 35 variety of *Salmonella* subgenera was constructed to

insure that the marker would include a broad range of *Salmonella* strains. The positive test panel contained of the following *Salmonella* serotypes: Subgenus I; *S. typhimurium*, *S. typhi*, *S. enteritidis*, *S. saintpaul*,
5 *S. binza*, *S. napolii*, *S. clerkwell*, *S. infantis*,
S. newport, *S. heidelberg*, *S. virchow*, *S. stanley*,
S. senftenberg, *S. gallinarium*, *S. cholerasuis*,
S. paratyphi, *S. bredeney*, *S. kedougou*, *S. montevideo*,
S. hadar, *S. panama*, *S. braenderup*, *S. blockley*,
10 *S. agona*, *S. brandenberg*, *S. anatum*, *S. thompson*,
S. berta, *S. manchester*, *S. ealing*, *S. eastbourne*,
S. indiana, *S. weltevreden*, *S. bracknell*,
S. bovismorbificans, *S. bareilly*, *S. bristol*, *S. bergen*,
S. berkeley, *S. birkinhead*, *S. austin*, *S. amager*,
15 *S. blukwa*, *S. bonn*, *S. brazil*, *S. butantan*,
S. bodjonegro, *S. adelaide*, *S. allandale*,
S. albuquerque, *S. aequatoria*, *abaetetube*, *S. alabama*,
S. alachua, and *S. chicago*; Subgenus II; *S. artis*,
S. bloemfontein, *S. bulawayo*, *S. bleadon*, *S. betioky*,
20 *S. basel*; Subgenus IIIa; *S. arizonae*; Subgenus V;
S. brookfield.

The negative test panel in the screening for a RAPD marker specific to *Salmonella* consisted of the following species; *Escherichia coli*, *Escherichia blattae*,
25 *Escherichia fergusonii*, *Escherichia hermani*, *Escherichia vulneris*, *Shigella sonnei*, *Shigella flexneri*, *Shigella dysenteriae*, *Shigella boydii*, *Citrobacter diversus*, and *Citrobacter freundii*. These species represent a
sampling of strains which are not included within the
30 genus *Salmonella* but are genetically similar to *Salmonella*. If strains representing these species show a substantially different RAPD pattern when amplified with the arbitrary primer used to generate the *Salmonella* marker, and if the selected *Salmonella* marker

is absent from the pattern, it is expected that the marker sequence will be selective for *Salmonella*.

EXAMPLE 1

ISOLATION OF DIAGNOSTIC FRAGMENT FROM *SALMONELLA* SP.

5 RAPD Screen Test Results:

Genomic DNA was isolated from members of both the positive and negative test panel members (above) and used to screen eight, 12-base primers of arbitrary sequence. These primers were used to generate RAPD
10 patterns for strains representing the positive and negative test panels. The primers used in the initial RAPD screening are listed in Table I.

TABLE I

Twelve-Base Arbitrary Primers Used in the
Generation of RAPD Patterns for the Purpose of
Identifying a Specific Genus Level *Salmonella* Marker

12CN01 -	AGC	TGA	TGC	TAC	(Sequence ID No. 2)
12CN02 -	AGT	CGA	ACT	GTC	(Sequence ID No. 3)
12CN03 -	TTA	GTC	ACG	GCA	(Sequence ID No. 4)
12CN04 -	TGC	GAT	ACC	GTA	(Sequence ID No. 5)
12CN05 -	CTA	CAG	CTG	ATG	(Sequence ID No. 6)
12CN06 -	GTC	AGT	CGA	ACT	(Sequence ID No. 7)
12CN07 -	GGC	ATT	AGT	CAC	(Sequence ID No. 8)
12CN08 -	CGT	ATG	CGA	TAC	(Sequence ID No. 9)

The primers were used individually and as mixed pairs in the following amplification protocol;

15 For each 50 μ l reaction, 2 μ l - dNTP mix (5 mM dNTP each), 35 μ l deionized water, 5 μ l - 10X reaction buffer (500 mM KCl, 100 mM tris @ pH 8.3, 15 mM MgCl₂, 0.003% gelatin), 2.5 μ l - each primer (10 mM) (5 μ l if only one primer is used), 0.4 μ l Taq polymerase (5 U/ μ l), and
20 1.2 μ l Taq dilution buffer (10 mM tris @ pH 8.0 and 1.0% Tween 20) were combined. 1.0 μ l - genomic bacterial DNA @ 50 ng/ μ l was added. The reaction was heated to 94°C

for 5 minutes. 32 cycles of the following temperature cycle were run; 1' @ 94°, 5' @ 46°, 2' ramp to 72°C, and 2' @ 72°C. A 5 µl aliquot of the reaction was combined with 2 µl of Ficol-loading buffer and run on a 4%

5 acrylamide gel (29:1)/1.0x TBE.

Figure 1A shows the RAPD patterns as separated by gel electrophoresis for samples of 16 different species of *Salmonella* from the positive test panel which was amplified with a single primer, 12CN03. The lanes are
10 correlated with the *Salmonella* species as follows:

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>S. typhimurium</i> 587 (ATCC 29057)	9	<i>S. infantis</i> 728
2	<i>S. typhimurium</i> 588 (ATCC 29631)	10	<i>S. heidelberg</i> 577
3	<i>S. binza</i> 1085	11	<i>S. virchow</i> 738
4	<i>S. napoli</i> 966	12	<i>S. stanley</i> 739
5	<i>S. enteritidis</i> 1109	13	<i>S. senftenberg</i> 740
6	<i>S. enteritidis</i> 737	14	<i>S. gallinarium</i> 741
7	<i>S. newport</i> 707 (ATCC 6962)	15	<i>S. cholerasuis</i> 917 (ATCC 13312)
8	<i>S. arizonae</i> 725 (ATCC 13314)	16	<i>S. paratyphi</i> A 918 (ATCC 9150)

Standard amplification conditions for amplification of DNA from the positive test panel consisted of 0.2 mM dNTPs, 1 µM 12CN03 primer and a reaction buffer of 50 mM KCl, 10 mM tris @ pH 8.3, 1.5 mM MgCl₂, and 0.0003%

15 gelatin. A total of 32 cycles were run under the following conditions: 1' at 94°C; 5' at 46°C; 2' ramp to 72°C and 2' at 72°C. The final cycle was followed by an additional 9' at 72°C. Unlabeled lanes contain molecular weight markers of the following sizes; 228,
20 412, 693, 1331, and 2306 base pairs (bp). RAPD amplification products were electrophoresed in 4% acrylamide/bisacrylamide (29/1) using a 1.0 X tris-

borate-EDTA running buffer for 55 minutes at a field strength of 14V/cm. Following electrophoresis the gels were stained for 15 minutes in a solution of ethidium bromide at 0.25 µg/ml.

- 5 As is evident by Figure 1A the positive test panel produced two characteristic amplification products of 800 and 2000 bp, which appeared in over 90% of the 91 *Salmonella* strains tested.

10 Figure 1B shows the RAPD patterns as separated by gel electrophoresis for samples of 13 different species of a variety of *Salmonella* bacteria from the negative test panel which were amplified with a single primer, 12CN03. The lanes are correlated with the bacterial species as follows:

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>Shigella sonnei</i> 702	9	<i>Escherichia coli</i> 90
2	<i>Shigella flexneri</i> 1083 (ATCC 29903)	10	<i>Escherichia blattae</i> 846 (ATCC 29907)
3	<i>Shigella dysenteriae</i> 1082 (ATCC 13313)	11	<i>Escherichia fergusonii</i> 847 (ATCC 35469)
4	<i>Shigella boydii</i> 1081 (ATCC 8700)	12	<i>Escherichia hermani</i> 848 (ATCC 33650)
5	<i>Citrobacter diversus</i> 97	13	<i>Escherichia vulneris</i> 850 (ATCC 33821)
6	<i>Citrobacter freundii</i> 383 (ATCC 8700)		

- 15 Standard amplification conditions for the amplification of the negative test panel consisted of 0.2 mM dNTPs, 1 µM 12CN03 primer and a reaction buffer of 50 mM KCl, 10 mM tris @ pH 8.3, 1.5 mM MgCl₂, and 0.0003% gelatin. A total of 32 cycles were run under
- 20 the following conditions: 1' at 94°C; 5' at 46°C; 2' ramp to 72°C and 2' at 72°C. The final cycle was followed by an additional 9' at 72°C. Molecular weight markers, gel composition, electrophoresis and staining

conditions were as described above for the positive test panel.

As is evident by the data in figure 1B, none of the negative test panel group showed the 800 bp or 2000 bp amplification products seen in the positive test panel.

5 Extraction and Sequencing of the *Salmonella* diagnostic Fragment:

The 800 bp product for *Salmonella typhimurium* 587 (ATCC #29057) was selected for extraction and

10 sequencing. The amplification product was isolated by electrophoresis in a low melting point agarose. The fragment was cut from the gel and extracted onto GlassMilk™ using a customized procedure from the

15 Geneclean kit sold by Bio 101 Inc. The fragment was then eluted and reamplified with the 12CN03 primer to provide quantities of DNA suitable for sequencing.

Since both ends of the fragment contain the same 12 base sequence, priming the parent diagnostic fragment with the 12CN03 primer would result in the production of

20 two simultaneous sequences superimposed upon each other, which could not be resolved into the individual single-stranded sequences. Hence, it was necessary to carry out a restriction endonuclease digestion of the

25 amplified 12CN03 product prior to running the sequencing reaction. Digest products were separated electrophoretically in low melting agarose and the

30 appropriate restriction product was reisolated using the Geneclean procedure. The individual purified restriction digest products were then sequenced using

30 12CN03 as a sequencing primer. The restriction fragments were sequenced by the Sanger chain-termination method using fluorescence-labeled dideoxynucleotides and the Genesis 2000™ DNA Analysis System.

An example of the sequencing protocol used is as

35 follows:

Combine 1.5 μ l - purified digest product (est. 100 ng), 3.5 μ l - 12CN03 @ 10.0 ng/ μ l and 28.5 μ l - H₂O and heat to 95°C for 2 minutes. Immediately place the mixture on wet ice. Add the following mixture 10 μ l -

5 5X reverse transcriptase reaction buffer (300 mM tris @ pH 8.3, 375 mM NaCl, 37.5 mM MgCl₂), 6.5 μ l - dNTP stock (180 μ M ea.), 0.65 μ l - ddNTP stock (250 μ M 505nm-ddGTP, 800 μ M 512nm-ddATP, 210 μ M 519nm-ddCTP and 700 μ M 526nm-ddTTP) and 1 μ l - reverse transcriptase. Vortex,

10 centrifuge and then incubate at 46°C for 15 minutes. Separate the sequencing products on a spin column and vacuum dry. Wash with 150 μ l of cold 70% ethanol and centrifuge 5 min. Vacuum dry and reconstitute in 3 μ l formamide.

15 The labeled sequencing products were then analyzed by the Genesis 2000™ DNA Analysis System. Once differential sequence had been determined at both ends of the *Salmonella* target fragment the remaining sequence information was obtained through the use of either

20 asymmetric PCR to generate single-stranded DNA or a modified double-stranded DNA sequencing protocol using double-stranded PCR product. The modification in the double-stranded protocol consisted of using a 46°C annealing temperature and a primer:template ratio of

25 25:1. This ratio is significantly higher than is generally practiced in sequencing reactions. At such a large primer:template ratio, priming at multiple sites is generally observed with single-stranded templates. However, when the template consists of short linear

30 double-stranded DNA, successful priming can only occur at 5' blunt ends of the template and only with a primer whose sequence matches that end. The net result is that only a single discrete sequencing product is observed under these conditions. The sequence of the complete

35 *Salmonella* fragment is shown in Figure 2.

EXAMPLE 2
DETERMINATION OF POLYMORPHIC
POSITIVE TEST PANEL STRAINS

5 The following procedure was used to determine which strains of *Salmonella* were most "polymorphic" with respect to the sequence of the diagnostic fragment shown in Figure 2. Two sets of amplification primer pairs were arbitrarily selected from the marker sequence. The sequence of these primers is shown in Table II.

TABLE II

Primers used in the determination of polymorphic *Salmonella*

#54-23	GAC	GCT	TAA	TGC	GGT	TAA	CGC	CA	(Sequence ID No. 10)
#126-23	AAC	CAT	GCA	TCA	TCG	GCA	GAA	CG	(Sequence ID No. 11)
#648rc-23	AGT	AGC	CTG	CCG	CTT	ACG	CTG	AA	(Sequence ID No. 12)
#665rc-23	TCA	GGA	TGC	AGG	CGA	TAG	TAG	CC	(Sequence ID No. 13)

10 Primer nomenclature:

The first number indicates the 3' position of the primer on the *Salmonella* target sequence in Figure 2. The rc indicates that the primer sequence is derived from the reverse complementary strand. The 23 indicates
 15 the length of the primer.

Amplifications were carried out on DNA isolated from 740 strains of *Salmonella* representing all six subgenus groups for each of the primer sets, 54-23/665rc-23 and 126-23/648rc/23. Standard
 20 amplification conditions consisted of 0.2 mM dNTPs, 0.5 μ M each primer and a reaction buffer of 50 mM KCl, 10 mM tris @ pH 8.3, 1.5 mM MgCl₂, and 0.0003% gelatin. A total of 35 cycles were run under the following conditions: 15 seconds at 94°C; 2 minutes at 69°C and
 25 1 minute at 72°C. The final cycle was followed by an additional 7 minutes at 72°C. Gel composition, electrophoresis and staining conditions were as

described above for the positive test panel in Example 1.

Strains of *Salmonella* were classified as a "polymorphic" if they produced amplification products that fell into the following categories:

- i) weak, inconsistent, or total lack of production of an amplification product;
- ii) amplification products which are larger or smaller than the generally observed amplification product;
- iii) the presence of more than one amplification product.

Examples of these types of polymorphic amplification events are shown in Figure 3. Figure 3 shows the amplification product patterns as separated by gel electrophoresis for samples of 6 polymorphic and 6 normal *Salmonella* amplified with the primers of Table II. The lanes are correlated with the *Salmonella* strains as follows:

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>S. arizonae</i> 1573	7	<i>S. Subgenus Group II</i> 1514
2	<i>S. arizonae</i> 1572	8	<i>S. Subgenus Group V</i> 1535
3	<i>S. typhimurium</i> 708 (ATCC 13311)	9	<i>S. Subgenus Group IV</i> 1714
4	<i>S. arizonae</i> 726 (ATCC 12324)	10	<i>S. Subgenus Group V</i> 1773
5	<i>S. oranienburg</i> 2212	11	<i>S. Subgenus Group I</i> 1513
6	<i>S. Subgenus Group I</i> 2213	12	<i>S. Subgenus Group I</i> 1517

From the original group of 740 *Salmonella* strains a group of 43 polymorphic *Salmonella* were selected.

EXAMPLE 3
EVALUATION OF PRIMING SITES WITHIN THE
DIAGNOSTIC FRAGMENT FOR THE BEST
GENUS LEVEL INCLUSIVITY OF SALMONELLA

5 Example 3 illustrates the method used to identify which priming sites within the diagnostic *Salmonella* fragment showed the best inclusivity for *Salmonella* at the genus level.

10 Primers were prepared for a large number sites at both ends of the *Salmonella* target sequence. Amplifications were carried out on genomic DNA from the 43 polymorphic *Salmonella* for a variety of these primer combinations according to the protocol listed below. In cases where a given primer combination produced an
15 amplification product in over 90% of the polymorphic *Salmonella*, additional primers were then prepared which moved one of the priming sites upstream or downstream one base at a time. Once the priming site that found the highest portion of polymorphic *Salmonella* was
20 identified, that site was fixed and then additional primers were prepared which moved the priming site at the other end of the *Salmonella* target sequence upstream or downstream one base at a time. The combination of priming sites which produced an amplification product
25 for the highest percentage of polymorphic *Salmonella* would then be evaluated at the next stage of the screening procedure.

 Primer-screening amplification reactions were conducted using the following procedure:

30 Combine 1.5 μ l - dNTP mix (5 mM each dNTP), 40 μ l - deionized water, 5 μ l - 10X reaction buffer (500 mM KCl, 100 mM tris @ pH 8.3, 15 mM MgCl₂, 0.003% gelatin)
 0.4 μ l - Taq polymerase (5U/ μ L), 1.2 μ l - Taq dilution buffer (10 mM tris @ pH 8.0 and 1.0% Tween 20), 0.66 μ l
35 - each primer (26-mer @ 10 μ M), and 1.0 μ l - genomic DNA

@ 50 ng/ μ l. Heat to 94°C for 2 minutes. Run 35 cycles of 15" @ 94°C; 3' @ 72°C. Combine a 5 μ l aliquot of the reaction with 2 μ l of Ficol-loading buffer and run on a 4% acrylamide gel (29:1)/1.0X TBE.

- 5 Sample responses were graded as follows:

If a PCR product was visible at $< 5 \times 10^4$ DNA copies per reaction the result was scored as +1.

If a PCR product was only visible when the DNA copy number was $> 5 \times 10^4$ copies per reaction the test was

- 10 scored as +0.5.

The scores for the 43 strains were summed and divided by 43. The results of the evaluation were assembled in Table III.

The numbers on the rows and columns represent the 3' positions relative to Sequence ID No. 1 of the two primers used in the amplification reaction. Based on the results of the primer site evaluation, four locations on the target sequence were sufficiently well conserved to yield priming sites capable of capturing over 95% of the polymorphic *Salmonella*. These sites were found in the following locations on the target sequence as displayed in Figure 2; 59-60, 534-536, 665 and 761. The 761 and 534 sites were selected over the 665 site because priming sites surrounding the 761 and 534 base positions detected a higher portion of the polymorphic *Salmonella*. Both the 59 and 60 sites were evaluated as possible priming sites for the complementary strand of the target. The sequences for these primers are shown in Table IV.

TABLE IV
Primer Sequences Found in at Least 95%
of the Polymorphic *Salmonella*

#59-26	TTA	GCC	GGG	ACG	CTT	AAT	GCG	GTT	AA	Sequence ID No. 14
#60-26	TAG	CCG	GGA	CGC	TTA	ATG	CGG	TTA	AC	Sequence ID No. 15
#534rc-26	CTA	TTT	TCT	GGC	CTG	ACG	CTA	TGA	CC	Sequence ID No. 16
#536rc-26	TTC	TAT	TTT	CTG	GCC	TGA	CGC	TAT	GA	Sequence ID No. 17
#665rc-26	CAT	TCA	GGA	TGC	AGG	CGA	TAG	TAG	CC	Sequence ID No. 18
#761rc-26	CTT	TAC	CGC	TTC	CAG	TGT	GGC	CTG	AA	Sequence ID No. 19

Primer nomenclature:

The first number indicates the 3' position of the primer on the *Salmonella* target sequence in Figure 2. The rc indicates that the primer sequence is derived from the reverse complementary strand. The 26 indicates the length of the primer.

EXAMPLE 4EVALUATION OF LARGER POPULATIONS OF
NEGATIVE AND POSITIVE TEST PANELS

5 Since the presence of bacteria in the genus *Salmonella* will be determined based on the production of an amplification product generated from the primers now being screened, it is necessary to conduct a broader sampling of strains representing the negative and positive test panels.

10 The selectivity of the *Salmonella* primer sets was evaluated by testing representatives of the following species representing the negative test panel to determine whether they contained DNA sequences which were amplifiable with either the 60-26/76lrc-26 primer
15 set or any combination of primers 59-26 or 60-26 with 534rc-26 or 536rc-26; *Escherichia coli*, *Shigella sonnei*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella boydii*, *Enterobacter cloacae*, *Enterobacter agglomerans*, *Enterobacter aerogenes*, *Citrobacter freundii*,
20 *Citrobacter diversus*, *Hafnia alvei*, *Proteus mirabilis*, *Proteus morganii*, *Proteus vulgaris*, *Klebsiella pneumoniae*, *Serratia marcescens*, *Yersinia enterocolitica*, *Listeria monocytogenes*, *Listeria innocua*, *Listeria ivanovii*, *Staphylococcus aureus*,
25 *Staphylococcus warneri*, *Staphylococcus saprophyticus*, *Staphylococcus epidermidis*, *Enterococcus faecalis*, *Bacillus cereus*, *Bacillus thuringiensis*, *Bacillus subtilis*.

A representative composite showing PCR
30 amplification products for the non-*Salmonella* strains listed below is shown in Figure 4. Figure 4 shows the amplification products formed using the 60-26/76lrc-26 primer set as separated by gel electrophoresis for samples of 44 non-*Salmonella*. Four strains of
35 *Salmonella* were also included in the reaction set as a

positive control to indicate that conditions were sufficient for amplification of the *Salmonella* target sequence to take place. The lanes are correlated with the non-*Salmonella* and *Salmonella* strains as follows:

A

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>Escherichia coli</i> 25	7	<i>Enterobacter cloacae</i> 123
2	<i>Escherichia coli</i> 33	8	<i>Enterobacter cloacae</i> 221
3	<i>Escherichia coli</i> 57	9	<i>Enterobacter cloacae</i> 313
4	<i>Escherichia coli</i> 84	10	<i>Enterobacter cloacae</i> 375 (ATCC 13047)
5	<i>Escherichia coli</i> 139	11	<i>Proteus mirabilis</i> 360
6	<i>Salmonella typhimurium</i> 897	12	<i>Proteus mirabilis</i> 364

B

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>Proteus morganii</i> 99	7	<i>Proteus vulgaris</i> 959
2	<i>Proteus morganii</i> 363	8	<i>Enterobacter agglomerans</i> 905
3	<i>Salmonella enteritidis</i> 1109	9	<i>Enterobacter aerogenes</i> 62
4	<i>Proteus vulgaris</i> 273	10	<i>Enterobacter aerogenes</i> 376 (ATCC 13048)
5	<i>Proteus vulgaris</i> 275	11	<i>Klebsiella pneumoniae</i> 373 (ATCC 13883)
6	<i>Proteus vulgaris</i> 385 (ATCC 13315)	12	<i>Klebsiella pneumoniae</i> 749

C

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>Listeria monocytogenes</i> 938	7	<i>Citrobacter freundii</i> 896
2	<i>Listeria monocytogenes</i> 941	8	<i>Citrobacter diversus</i> 217
3	<i>Listeria innocua</i> 1157	9	<i>Hafnia alvei</i> 934
4	<i>Listeria ivanovii</i> 1167	10	<i>Serratia marcesens</i> 372
5	<i>Salmonella infantis</i> 908	11	<i>Enterococcus faecalis</i> 283 (ATCC 19433)
6	<i>Citrobacter freundii</i> 361	12	<i>Yersinia enterocolitica</i> 750

37

D

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>Staphylococcus aureus</i> 118	7	<i>Staphylococcus saprophyticus</i> 788
2	<i>Staphylococcus aureus</i> 207	8	<i>Salmonella saintpaul</i> 1086
3	<i>Staphylococcus aureus</i> 610	9	<i>Shigella sonnei</i> 701
4	<i>Staphylococcus aureus</i> 812	10	<i>Shigella boydii</i> 1081 (ATCC 8700)
5	<i>Staphylococcus warneri</i> 793	11	<i>Shigella dysenteriae</i> 1082 (ATCC 13313)
6	<i>Staphylococcus saprophyticus</i> 762	12	<i>Shigella flexneri</i> 1083 (ATCC 29903)

Of the 100 strains which were evaluated only one strain which was tentatively identified as *Hafnia alvei*, gave a false positive result with the 60-26 and 761rc-26 primer set. The identity of this false positive is considered ambiguous because although its ribotyping pattern appears to be closer to *Hafnia alvei* than to the genus *Salmonella*, the strain appears to be biochemically closer to *Salmonella*. The remaining 35 strains of *Hafnia alvei*, which were screened all tested negative for the presence of the *Salmonella* test sequence. Primer combinations using 3' sites at base positions 59 or 60 along with complementary strand priming sites at 534 or 536 all generated amplification products with at least 20% of the negative test panel. Since this rate of false positives was unacceptable for use in the preferred embodiments only the 60-26 and 761rc-26 primer set was selected for the further evaluation. The fragment of Figure 2 flanked and included by these primers included nucleic acid bases starting at position 35 and ending at position 786; this is the diagnostic target of the invention for *Salmonella*. Position 35 to 786 of Sequence ID No. 1 is designated Sequence ID No. 21. Position 35 to 786 of Sequence ID No. 20 is designated as Sequence ID No. 22.

The detection efficiency of the diagnostic marker primers 60-26 and 761rc-26 primers was then evaluated on a test group of over 1480 *Salmonella* strains. A breakdown of the test group by subgenus group and 5 serotype is shown in Table V.

TABLE V
List of *Salmonella* Serotypes Comprising the Test Group
for the 60-26 and 761rc-26 Primers

Serotype/Subgenus	No.	Serotype/Subgenus	No.
<i>Salmonella</i> abaetetuba F	3	<i>Salmonella</i> london E1	2
<i>Salmonella</i> adabraka E1	1	<i>Salmonella</i> madelia H	2
<i>Salmonella</i> adelaide O	11	<i>Salmonella</i> manchester C2	3
<i>Salmonella</i> agama B	2	<i>Salmonella</i> manhattan C2	5
<i>Salmonella</i> agona O	25	<i>Salmonella</i> manila E2	2
<i>Salmonella</i> ajiobo G2	2	<i>Salmonella</i> mbandaka C1	14
<i>Salmonella</i> alabama D1	2	<i>Salmonella</i> meleagridis E1	3
<i>Salmonella</i> albany C3	5	<i>Salmonella</i> minnesota L	5
<i>Salmonella</i> altendorf B	2	<i>Salmonella</i> mississippi G2	4
<i>Salmonella</i> amsterdam E1	7	<i>Salmonella</i> montevideo C1	9
<i>Salmonella</i> anatum E1	42	<i>Salmonella</i> morehead N	2
<i>Salmonella</i> arechavaleta B	2	<i>Salmonella</i> muenchen C2	11
<i>Salmonella</i> arkansas E3	11	<i>Salmonella</i> muenster E1	10
<i>Salmonella</i> austin C1	2	<i>Salmonella</i> napoli D1	7
<i>Salmonella</i> bareilly C1	8	<i>Salmonella</i> newbrunswick E2	5
<i>Salmonella</i> berta D1	13	<i>Salmonella</i> newington E2	1
<i>Salmonella</i> binza E2	19	<i>Salmonella</i> newport C2	26
<i>Salmonella</i> blockley C2	4	<i>Salmonella</i> nyborg E1	2
<i>Salmonella</i> bodjonegoro N	2	<i>Salmonella</i> ohio C1	53
<i>Salmonella</i> braenderup C1	30	<i>Salmonella</i> oranienburg C1	8
<i>Salmonella</i> brandenburg B	9	<i>Salmonella</i> othmarschen C1	5
<i>Salmonella</i> bredeney B	14	<i>Salmonella</i> panama D1	8
<i>Salmonella</i> california B	7	<i>Salmonella</i> paratyphi A	1
<i>Salmonella</i> cerro K	13	<i>Salmonella</i> poona G1	2
<i>Salmonella</i> champaign Q	2	<i>Salmonella</i> pullorum D1	21
<i>Salmonella</i> chandans F	5	<i>Salmonella</i> reading B	8

<i>Salmonella choleraesuis</i> C1	13	<i>Salmonella redlands</i> I	2
<i>Salmonella corvallis</i> C3	6	<i>Salmonella rostock</i> D1	2
<i>Salmonella cubana</i> G2	21	<i>Salmonella rubislaw</i> F	5
<i>Salmonella daressalaam</i> B	1	<i>Salmonella saintpaul</i> B	10
<i>Salmonella derby</i> B	8	<i>Salmonella sandiego</i> B	7
<i>Salmonella drypool</i> E2	11	<i>Salmonella santiago</i> C3	48
<i>Salmonella dublin</i> D1	14	<i>Salmonella schwarzengr.</i> B	10
<i>Salmonella durham</i> G2	5	<i>Salmonella sculcoates</i>	2
<i>Salmonella ealing</i> O	3	<i>Salmonella senftenberg</i> E4	56
<i>Salmonella enteritidis</i> D1	124	<i>Salmonella sladun</i> B	2
<i>Salmonella eschweiler</i> C1	2	<i>Salmonella stanley</i> B	7
<i>Salmonella ferlac</i> H	2	<i>Salmonella stanleyville</i> B	3
<i>Salmonella gallinarum</i> O	3	<i>Salmonella sya</i> X	4
<i>Salmonella give</i> E1	4	<i>Salmonella tennessee</i> C1	19
<i>Salmonella haardt</i> O	12	<i>Salmonella thomasville</i> E3	11
<i>Salmonella hadar</i> C2	17	<i>Salmonella thompson</i> C1	16
<i>Salmonella havana</i> G2	15	<i>Salmonella typhi</i> D1	2
<i>Salmonella heidelberg</i> B	20	<i>Salmonella typhimurium</i> B	97
<i>Salmonella indiana</i> B	13	<i>Salmonella urbana</i> N	2
<i>Salmonella infantis</i> C1	31	<i>Salmonella virchow</i> C1	14
<i>Salmonella johannesburg</i> R	5	<i>Salmonella waycross</i> S	2
<i>Salmonella kedougou</i> G2	7	<i>Salmonella worthington</i> G2	11
<i>Salmonella kentucky</i> C3	11	<i>Salmonella</i> Group I species	211
<i>Salmonella kiambu</i> B	2	<i>Salmonella</i> Group II species	23
<i>Salmonella krefeld</i> E4	2	<i>Salmonella</i> Group IIIa species	39
<i>Salmonella kubacha</i> B	4	<i>Salmonella</i> Group IIIb species	19
<i>Salmonella lexington</i> E1	7	<i>Salmonella</i> Group IV species	16
<i>Salmonella lille</i> C1	8	<i>Salmonella</i> Group V species	2
<i>Salmonella livingston</i> C1	9		

This pair of priming sites proved to be extremely accurate in detecting *Salmonella* strains from all six subgenus groups in the genus *Salmonella*. The 1390 strains of Group I *Salmonella* were detected at an efficiency of 99.75%. Although the remaining five

subgenus groups contained considerably fewer strains, the strains comprising all these groups were detected at 100% efficiency. The detection efficiency of the 60 and 761 priming sites for the individual subgenus groups and the entire *Salmonella* test group are shown in Table VI.

TABLE VI

Summary of *Salmonella* Detecting Efficiency
for the 60-26 and 761rc-26 Primer Set

Total Subgenus Group I Tested	1390
Total Positive	1386.5
% Positive	99.75
Total Subgenus Group II Tested	23
Total Positive	23
% Positive	100
Total Subgenus Group IIIa Tested	39
Total Positive	39
% Positive	100
Total Subgenus Group IIIb Tested	19
Total Positive	19
% Positive	100
Total Subgenus Group IV Tested	16
Total Positive	16
% Positive	100
Total Subgenus Group V Tested	2
Total Positive	2
% Positive	100
Total <i>Salmonella</i> Tested	1489
Total <i>Salmonella</i> Positive	1485.5
% Positive	99.76

If a PCR product was visible at $< 5 \times 10^4$ DNA copies per reaction the result was scored as +1.

If a PCR product was only visible when the DNA copy number was $> 5 \times 10^4$ copies per reaction the test was

5 scored as +0.5.

A representative composite showing PCR amplification products for the *Salmonella* strains listed below is shown in Figure 5.

10 Figure 5 shows the amplification products formed using the 60-26/761rc-26 primer set as separated by gel electrophoresis for samples of 44 *Salmonella*. The lanes are correlated with *Salmonella* strains as follows:

A

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>Salmonella</i> abaetetuba 1550	7	<i>Salmonella</i> anatum 1501
2	<i>Salmonella</i> adabraka 2340	8	<i>Salmonella</i> anatum 2744
3	<i>Salmonella</i> agona 1353	9	Blank
4	<i>Salmonella</i> agona 1446	10	<i>Salmonella</i> binza 1432
5	<i>Salmonella</i> agona 2339	11	<i>Salmonella</i> binza 2682
6	<i>Salmonella</i> altendorf 1654	12	<i>Salmonella</i> brandenburg 1355

B

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>Salmonella</i> enteritidis 706 (ATCC 6962)	7	<i>Salmonella</i> hadar 1231
2	<i>Salmonella</i> enteritidis 890	8	<i>Salmonella</i> havana 2245
3	<i>Salmonella</i> eschweiller 1647	9	<i>Salmonella</i> havana 2271
4	<i>Salmonella</i> gallinarum 1635	10	Blank
5	<i>Salmonella</i> gallinarum 2350	11	<i>Salmonella</i> heidelberg 1238
6	<i>Salmonella</i> haardt 1344	12	<i>Salmonella</i> heidelberg 1239

C

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>Salmonella</i> indiana 1480	7	<i>Salmonella</i> kentucky 2195
2	<i>Salmonella</i> infantis 727	8	<i>Salmonella</i> kentucky 2756
3	Blank	9	<i>Salmonella</i> kentucky 2759

42

4	<i>Salmonella infantis</i> 1437	10	<i>Salmonella kentucky</i> 2769
5	<i>Salmonella kedougou</i> 1251	11	<i>Salmonella kiambu</i> 919
6	<i>Salmonella kedougou</i> 1254	12	<i>Salmonella lexington</i> 1649

D

<u>Lane</u>	<u>Species and I.D. No.</u>	<u>Lane</u>	<u>Species and I.D. No.</u>
1	<i>Salmonella typhimurium</i> 1253	7	<i>Salmonella virchow</i> 1256
2	<i>Salmonella typhimurium</i> 1499	8	<i>Salmonella virchow</i> 1370
3	<i>Salmonella typhimurium</i> 1509	9	<i>Salmonella virchow</i> 1431
4	<i>Salmonella urbana</i> 1663	10	Blank
5	<i>Salmonella virchow</i> 738	11	<i>Salmonella worthington</i> 2638
6	<i>Salmonella virchow</i> 1241	12	<i>Salmonella vrindaban</i> 2314

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: E. I. DU PONT DE NEMOURS AND COMPANY
 - (B) STREET: 1007 MARKET STREET
 - (C) CITY: WILMINGTON
 - (D) STATE: DELAWARE
 - (E) COUNTRY: UNITED STATES OF AMERICA
 - (F) POSTAL CODE (ZIP): 19898
 - (G) TELEPHONE: 302-892-8112
 - (H) TELEFAX: 302-773-0164
 - (I) TELEX: 6717325
- (ii) TITLE OF INVENTION: SELECTION OF DIAGNOSTIC GENETIC MARKERS IN MICROORGANISMS AND USE OF A SPECIFIC MARKER FOR DETECTION OF SALMONELLA
- (iii) NUMBER OF SEQUENCES: 22
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: DISKETTE, 3.50 INCH
 - (B) COMPUTER: MACINTOSH
 - (C) OPERATING SYSTEM: MACINTOSH, 6.0
 - (D) SOFTWARE: MICROSOFT WORD, 4.0
- (v) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: GEIGER, KATHLEEN W.
 - (B) REGISTRATION NUMBER: 35,880
 - (C) REFERENCE/DOCKET NUMBER: MD-1068

44

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TTAGTCACGG CAGCCGCGAG GATGATATGG ATGTTAGCCG GGACGCTTAA TGCGGTAAAC   60
GCCATGCCGA CACCAGCGCC CGCCAGCGTG CCGAAACTGT AGAAACCATG CATCATCGGC   120
AGAACGTTTT TATTCAGCTC GCGTTCGACC GCCGCGCCTT CGACATTAAT CGCCACTTCG   180
GCGGCGCCAA AACTGGCGCC GAAAACGGCT AATCCAAGGG CAAAATCAG CGGCGAGGCG   240
CACCACAGCG CGACGCTAAG AATAACCATC CCGGTTACTG CACAGGTCAT CGTCGTGCGA   300
ATAACCTTCC GGGTGCCAAA TCGTTTCACC AGCCAGGCGG AACAAAGAAT ACCGCTCATT   360
GAACCGATAG AAAGCCCGAA TAAGACCGCC CCCATTTCCG CGGTAGAGAC GGAAAGAATA   420
TCCCGAATAG CAGGCGTTCG GGTGCCCAG GAGGCCATCA GCAGTCCGGG TAAAAAGAAG   480
AACATAAACA GCGCCCAGGT ACGGCGTTTT AAGGCGTTAC GTGAGGAGAG GACGGTCATA   540
GCGTCAGGCC AGAAAATAGA AGCGAGAGGT AACATTAGC AAGCTTGTGT ACATTTGTAC   600
ATATCATCGT CATACTTCAT TGTGCAGACA GTTTTACTG TCTGTTTTTT CAGCGTAAGC   660
GGCAGGCTAC TATCGCCTGC ATCCTGAATG AGATGTGGAA CTCATCATGA AAGAAAATGC   720
CGTAAGCGCG CCAATGATCC TAAGCGACGG GAAAAAATAA TTCAGGCCAC ACTGGAAGCG   780
GTAAAGACCT ATGGCACTCT GCCGTGACTA A                                     811

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGCTGATGCT AC

12

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGTCGAACTG TC

12

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTAGTCACGG CA

12

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGCGATACCG TA

12

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
CTACAGCTGA TG 12
- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
GTCAGTCGAA CT 12
- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
GGCATTAGTC AC 12
- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
CGTATGCGAT AC 12
- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
GACGCTTAAT GCGGTTAACG CCA 23
- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
AACCATGCAT CATCGGCAGA ACG 23
- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
AGTAGCCTGC CGCTTACGCT GAA 23
- (2) INFORMATION FOR SEQ ID NO:13:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
TCAGGATGCA GGCGATAGTA GCC 23
- (2) INFORMATION FOR SEQ ID NO:14:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs

48

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTAGCCGGGA CGCTTAATGC GGTAA

26

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAGCCGGGAC GCTTAATGCG GTTAAC

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTATTTTCTG GCCTGACGCT ATGACC

26

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCTATTTTC TGGCCTGACG CTATGA

26

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CATTACAGGAT GCAGGCGATA GTAGCC

26

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTTTACCGCT TCCAGTGTGG CCTGAA

26

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 811 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTAGTCACGG CAGAGTGCCA TAGGTCTTTA CCGCTTCCAG TGTGGCCTGA ATTATTTTTT 60
 CCCGTCGCTT AGGATCATTG GCGCGCTTAC GGCATTTTCT TTCATGATGA GTTCCACATC 120
 TCATTACAGGA TGCAGGCGAT AGTAGCCTGC CGCTTACGCT GAAAAAACAG ACAGTAAAAA 180
 CTGTCTGCAC AATGAAGTAT GACGATGATA TGTACAAATG TACACAAGCT TGCTAATGTT 240
 TACCTCTCGC TTCTATTTTC TGGCCTGACG CTATGACCGT CCTCTCCTCA CGTAACGCCT 300
 TAAAACGCCG TACCTGGGCG CTGTTTATGT TCTTCTTTT ACCCGGACTG CTGATGGCCT 360
 CCTGGGCAAC CCGAACGCCT GCTATTCGGG ATATTCTTTC CGTCTCTACC GCGGAAATGG 420

50

GGGCGGTCTT ATTCGGGCTT TCTATCGGTT CAATGAGCGG TATTCTTTGT TCCGCCTGGC 480
 TGGTGAAACG ATTTGGCACC CGGAAGGTTA TTCGCACGAC GATGACCTGT GCAGTAACCG 540
 GGATGGTTAT TCTTAGCGTC GCGCTGTGGT GCGCCTCGCC GCTGATTTTT GCCCTTGGAT 600
 TAGCCGTTTT CGGCGCCAGT TTTGGCGCCG CCGAAGTGGC GATTAATGTC GAAGGCGCGG 660
 CGGTGGAACG CGAGCTGAAT AAAACCGTTC TGCCGATGAT GCATGGTTTC TACAGTTTCG 720
 GCACGCTGGC GGGCGCTGGT GTCGGCATGG CGTTAACCGC ATTAAGCGTC CCGGCTAACA 780
 TCCATATCAT CCTCGCGGCT GCCGTGACTA A 811

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TAGCCGGGAC GCTTAATGCG GTTAACGCCA TGCCGACACC AGCGCCCGCC AGCGTGCCGA 60
 AACTGTAGAA ACCATGCATC ATCGGCAGAA CGGTTTTATT CAGCTCGCGT TCGACCGCCG 120
 CGCCTTCGAC ATTAATCGCC ACTTCGGCGG CGCCAAAACT GGCGCCGAAA ACGGCTAATC 180
 CAAGGGCAAA AATCAGCGGC GAGGCGCACC ACAGCGCGAC GCTAAGAATA ACCATCCCGG 240
 TTACTGCACA GGTCATCGTC GTGCGAATAA CCTTCCGGGT GCCAAATCGT TTCACCAGCC 300
 AGGCGGAACA AAGAATACCG CTCATTGAAC CGATAGAAAG CCCGAATAAG ACCGCCCCCA 360
 TTTCCGCGGT AGAGACGGAA AGAATATCCC GAATAGCAGG CGTTCGGGTT GCCCAGGAGG 420
 CCATCAGCAG TCCGGGTAAA AAGAAGAACA TAAACAGCGC CCAGGTACGG CGTTTTAAGG 480
 CGTTACGTGA GGAGAGGACG GTCATAGCGT CAGGCCAGAA AATAGAAGCG AGAGGTAAAC 540
 ATTAGCAAGC TTGTGTACAT TTGTACATAT CATCGTCATA CTTTATTGTG CAGACAGTTT 600
 TTACTGTCTG TTTTTCAGC GTAAGCGGCA GGCTACTATC GCCTGCATCC TGAATGAGAT 660
 GTGGAATCA TCATGAAAGA AAATGCCGTA AGCGCGCCAA TGATCCTAAG CGACGGGAAA 720
 AAATAATTCA GGCCACACTG GAAGCGGTAA AG 752

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs

51

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTTTACCGCT	TCCAGTGTGG	CCTGAATTAT	TTTTTCCCGT	CGCTTAGGAT	CATTGGCGCG	60
CTTACGGCAT	TTTCTTTCAT	GATGAGTTCC	ACATCTCATT	CAGGATGCAG	GCGATAGTAG	120
CCTGCCGCTT	ACGCTGAAAA	AACAGACAGT	AAAAACTGTC	TGCACAATGA	AGTATGACGA	180
TGATATGTAC	AAATGTACAC	AAGCTTGCTA	ATGTTTACCT	CTCGCTTCTA	TTTTCTGGCC	240
TGACGCTATG	ACCGTCCTCT	CCTCACGTAA	CGCCTTAAAA	CGCCGTACCT	GGGCGCTGTT	300
TATGTTCTTC	TTTTTACCCG	GACTGCTGAT	GGCCTCCTGG	GCAACCCGAA	CGCCTGCTAT	360
TCGGGATATT	CTTTCCTCT	CTACCGCGGA	AATGGGGGCG	GTCTTATTCG	GGCTTTCTAT	420
CGGTTCAATG	AGCGGTATTC	TTTGTTCCGC	CTGGCTGGTG	AAACGATTTG	GCACCCGGAA	480
GGTTATTCGC	ACGACGATGA	CCTGTGCAGT	AACCGGGATG	GTTATTCTTA	GCGTCGCGCT	540
GTGGTGCGCC	TCGCCGCTGA	TTTTTGCCCT	TGATTAGCC	GTTTTCGGCG	CCAGTTTTTG	600
CGCCGCCGAA	GTGGCGATTA	ATGTCGAAGG	CGCGGCGGTC	GAACGCGAGC	TGAATAAAAC	660
CGTTCTGCCG	ATGATGCATG	GTTTCTACAG	TTTCGGCACG	CTGGCGGGCG	CTGGTGTCGG	720
CATGGCGTTA	ACCGCATTAA	GCGTCCCGGC	TA			752

WHAT IS CLAIMED IS:

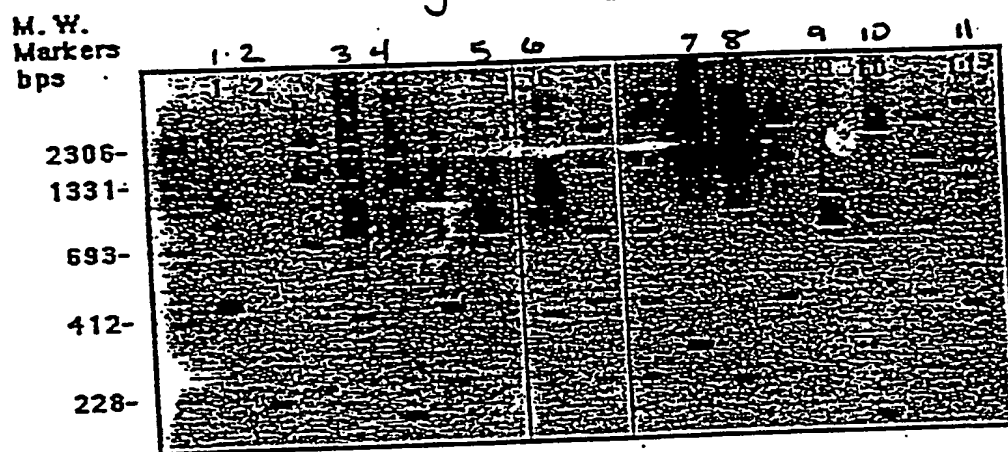
1. A method of determining whether an unknown bacterium is a member of the genus *Salmonella*, comprising analyzing the genomic DNA of said unknown bacterium to detect the presence of nucleic acid Sequence ID No. 1 or Sequence ID No. 20.
2. The method of Claim 1 wherein said analysis comprises the steps of:
 - (i) performing a PCR amplification reaction on the genomic DNA of said unknown bacterium using a pair of primers comprising a first primer and a second primer wherein said first primer has a nucleic acid sequence derived from Sequence ID No. 1 and said second primer has a nucleic acid sequence derived from Sequence ID No. 20; and
 - (ii) detecting the presence of DNA which has been amplified by said primer pair of step (i);whereby the presence of amplified DNA at step (ii) indicates that said unknown bacterium is a member of the genus *Salmonella*.
3. The method of Claim 2 wherein at step (i) said first primer is selected from the group consisting of Sequence ID Nos. 14 and 15, and said second primer is selected from the group consisting of Sequence ID Nos. 16, 17, 18, and 19.
4. The method of Claim 2 wherein at step (i) said first primer is Sequence ID No. 15 and said second primer is Sequence ID No. 19.
5. The method of Claim 1 wherein said analysis comprises contacting the genomic DNA of said unknown organism with a nucleic acid probe wherein said probe consists essentially of a nucleic acid sequence which is

complimentary to Sequence ID Nos. 1 or 20, or a fragment thereof, and further, detecting the presence of said hybridized probe.

6. An isolated nucleic acid fragment having
5 Sequence ID No. 1 or a fragment thereof.
7. An isolated nucleic acid fragment having
Sequence ID No. 20 or a fragment thereof.
8. An isolated nucleic acid fragment having
Sequence ID No. 14.
- 10 9. An isolated nucleic acid fragment having
Sequence ID No. 15.
10. An isolated nucleic acid fragment having
Sequence ID No. 16.
11. An isolated nucleic acid fragment having
15 Sequence ID No. 17.
12. An isolated nucleic acid fragment having
Sequence ID No. 18.
13. An isolated nucleic acid fragment having
Sequence ID No. 19.
- 20 14. An isolated nucleic acid fragment having
Sequence ID No. 21.
15. An isolated nucleic acid fragment having
Sequence ID No. 22.
16. An isolated nucleic acid fragment having
25 Sequence ID No. 4.

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Figure 1B



5		Seq. ID No 14	Seq. ID No 15	
	TTAGTCACGG CAGCCGCGAG GATGATATGG ATGTTAGCCG GGACGCTTAA TCGGGTTAHC			60
	AATCAGTGCC GTCGGCGCTC CTACTATACC TACAATCGGC CCTGCGAATT ACGCCAATTG			
10	GCCATGCCGA CACCAGCGCC CGCCAGCGTG CCGAAACTGT AGAAACCATG CATCATCGGC			120
	CGGTACGGCT GTGGTCGCGG GCGGTCGCAC GGCTTTGACA TCTTTGGTAC GTAGTAGCCG			
	AGAACGGTTT TATTAGCTC GCGTTCGACC GCCGCGCCTT CGACATTAAAT CGCCACTTCG			180
	TCTTGCCAAA ATAAGTCGAG CGCAAGCTGG CGGCGCGGAA GCTGTAATTA GCGGTGAAGC			
15	GCGGCGCCAA AACTGGCGCC GAAAACGGCT AATCCAAGGG CAAAATCAG CGGCGAGGCG			240
	CGCCGCGGTT TTGACCGCGG CTTTGGCCGA TTAGGTTCCC GTTTTATAGTC GCCGCTCCGC			
	CACCACAGCG CGACGCTAAG AATAACCATC CCGGTTACTG CACAGGTCAT CGTCGTGCGA			300
20	GTGGTGTCGC GCTGCGATTG TTATTGGTAG GGCCAATGAC GTGTCCAGTA GCAGCACGCT			
	ATAACCTTCC GGGTGCCAAA TCGTTTCACC AGCCAGGCGG AACAAAGAAT ACCGCTCATT			360
	TATTGGAAGG CCCACGGTTT AGCAAAGTGG TCGGTCCGCC TTGTTTCTTA TGGCGAGTAA			
25	GAACCGATAG AAAGCCCGAA TAAGACCGCC CCCATTTCCG CGGTAGAGAC GGAAAGAATA			420
	CTTGGCTATC TTTGGGGCTT ATTCTGGCGG GGGTAAAGGC GCCATCTCTG CCTTTCTTAT			
	TCCCGAATAG CAGGCGTTTCG GGTGCCCCAG GAGGCCATCA GCAGTCCGGG TAAAAGAAG			480
	AGGGCTTATC GTCCGCAAGC CCAACGGGTC CTCCGGTAGT CGTCAGGCCC ATTTTCTTTC			
30	AACATAAACA GCGCCCAGGT ACGGCGTTTT AAGGCGTTAC GTGAGGAGAG GACGGTCATA			540
	TTGTATTGT CGCGGGTCCA TGCCGCAAAA TTCCGCAATG CACTCCTCTC CTGCCAGTAT			
	CGGTCAGGCC AGAAAATAGA AGCGAGAGGT AAACATTAGC AAGCTTGTGT ACATTTGTAC			600
35	CGCAGTCCGG TCTTTTATCT TCGCTCTCCA TTTGTAATCG TTCGAACACA TGTAACATG			
	Seq. ID No 16	Seq. ID No 17		

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CR-

Figure 2B

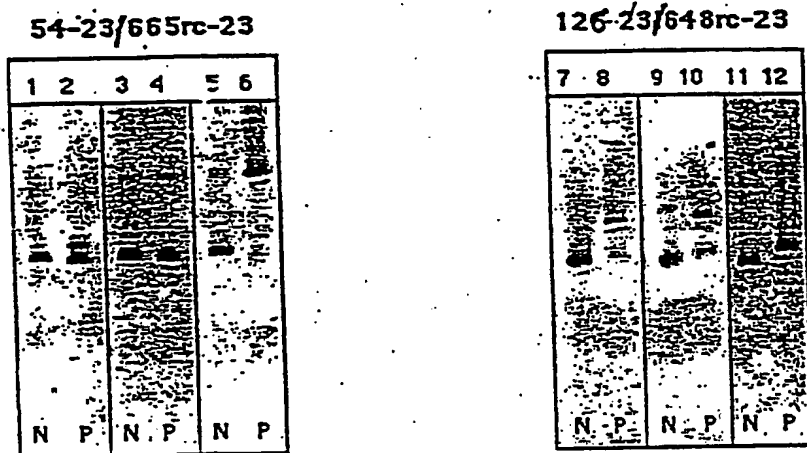
ATATCATCGT CATACTTCAT TGTCAGACA GTTTTACTG TCTGTTTTT CAGCGTAAGC 660
 TATAGTAGCA GTATGAAGTA ACACGTCGT CAAAATGAC AGACAAAAA GTCGCATTGC
 5 GGCAGGCTAC TATCGCCTGC ATCCTGAATG AGATGTGGAA CTCATCATGA AAGAAAATGC 720
 CCGTDCGATG ATAGCGGACG TAGGACTTAC TCTACACCTT GAGTAGTACT TTCITTTTACG
 Seq. ID No 18 ↑
 CGTAAGCGCG CCAATGATCC TAAGCGACGG GAAAAATAA TTCAGGCCAC ACTGGAAGCG 780
 GCATTGCGGC GGTACTAGG ATTCGCTGCC CTTTTTATT AAGTCCGGIG TGACCTTCGC
 10 Seq. ID No 19 ↑
 GTAAAGACCT ATGGCACTCT GCCGTGACTA A ← Sequence ID No 1
 CATTTGTGGA TACCGTGAGA CGGCACTGAT T ← Sequence ID No 20
 790 800 810
 15

Sequence ID No. 21 is basepair no. 35 to 786
of Sequence ID No 1.

Sequence ID No 22 is basepair no 786 to 35
of Sequence ID No 20.

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Figure 3



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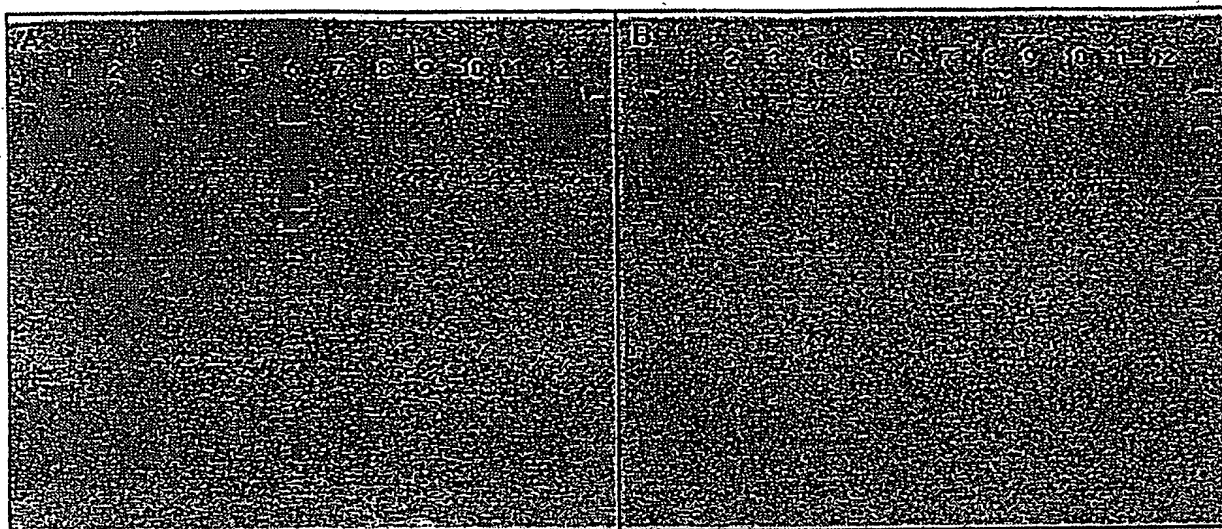


FIGURE 4A & 4B

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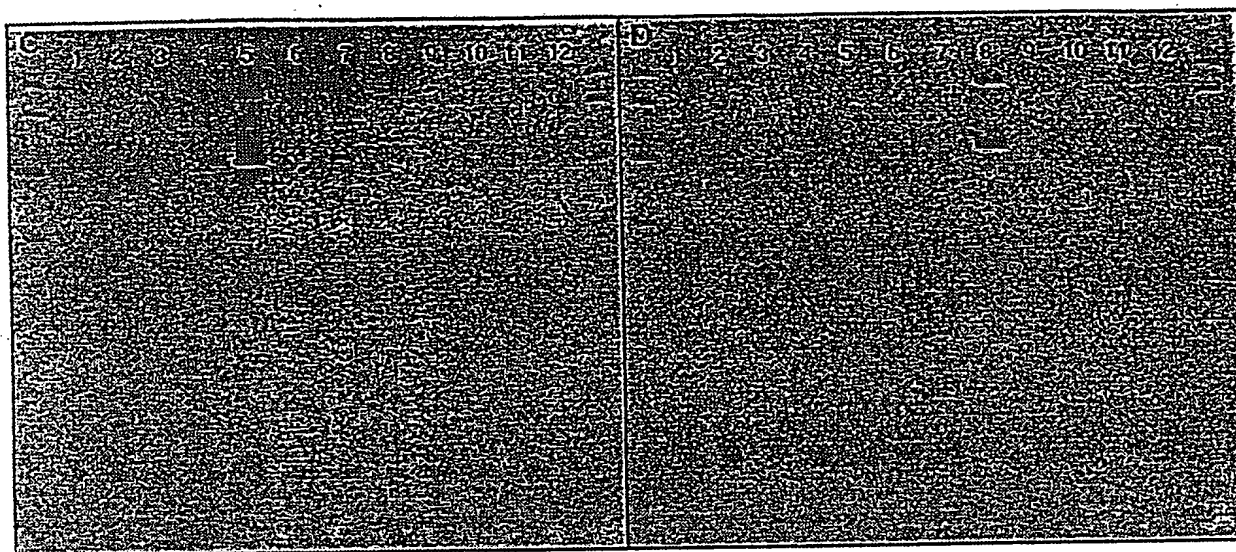


FIGURE 4C & 4D

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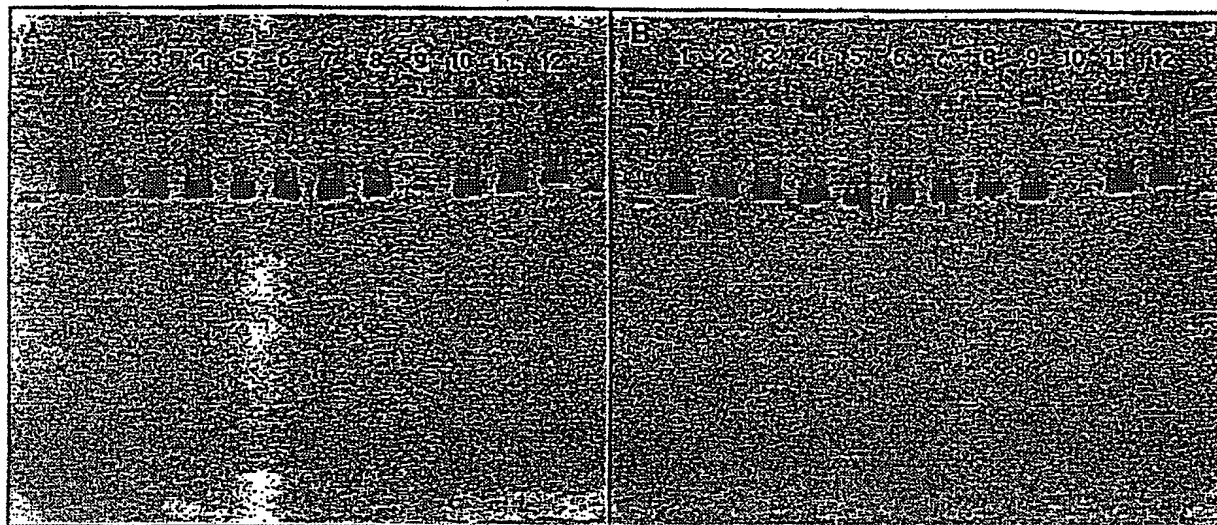


FIGURE 5A & 5B

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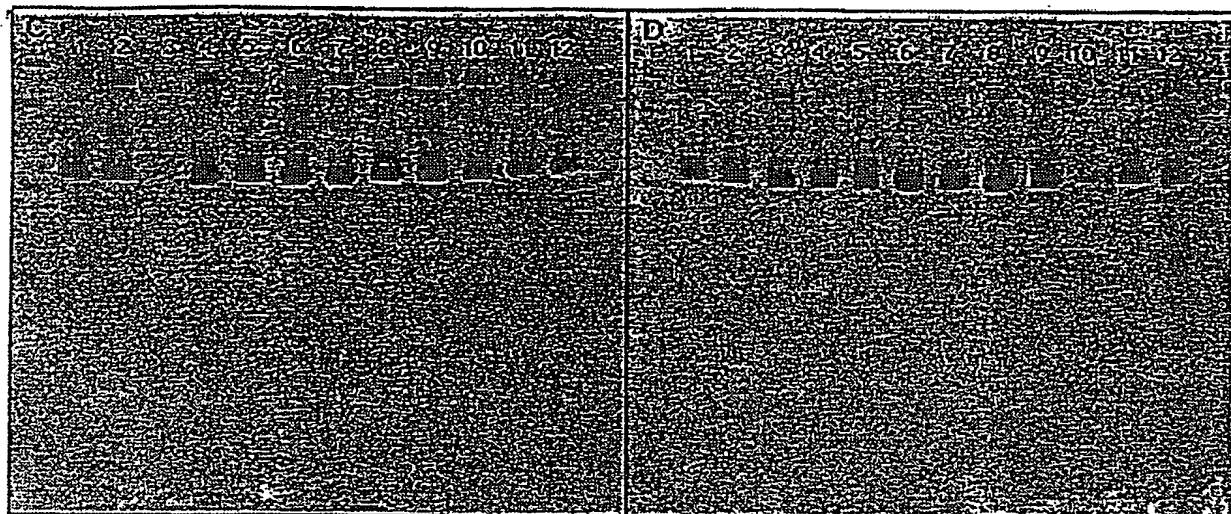


FIGURE 5C & 5D

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 95/06704

A. CLASSIFICATION OF SUBJECT MATTER

IPC6: C12Q 1/68, C12N 15/11 // C12Q 1/68, C12R 1:42
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC6: C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPOQUE, PAJ, WPI, CLAIMS, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO, A1, 9413832 (E.I. DU PONT DE NEMOURS AND COMPANY), 23 June 1994 (23.06.94), see the whole document, especially claim 16 --	1-16
X	WO, A1, 9304202 (WASHINGTON UNIVERSITY), 4 March 1993 (04.03.93), the whole document especially page 14, line 3 - line 25; page 18, line 13 - line 25 --	1-16
X	EP, A2, 0395292 (BARRY, THOMAS GERARD), 31 October 1990 (31.10.90), see the whole document and page 2, line 53 - page 3, line 17 --	1-16



Further documents are listed in the continuation of Box C.



See patent family annex.

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Date of the actual completion of the international search

21 Sept 1995

Date of mailing of the international search report

21-11-95

Name and mailing address of the International Searching Authority



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Authorized officer

PATRICK ANDERSSON

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 95/06704

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>WO, A1, 8905359 (INTEGRATED GENETICS, INC.), 15 June 1989 (15.06.89), see the whole document especially claims 1-2</p> <p style="text-align: center;">-- -----</p>	1-16

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/US 95/06704

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO-A1-	9413832	23/06/94	NONE		
WO-A1-	930420	04/03/93	AU-A-	2509592	16/03/93
EP-A2-	0395292	31/10/90	AU-B-	630932	12/11/92
			AU-A-	5365290	25/10/90
			JP-A-	3130099	03/06/91
WO-A1-	8905359	15/06/89	AU-A-	2932889	05/07/89
			EP-A, A-	0389564	03/10/90
			US-A-	5147778	15/09/92

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